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Ladas & Parry
26 West 61st Street
New York, NY 10023

EXAMINER

SAMSON, MARIA TERESA D

ART UNIT	PAPER NUMBER
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1638

DATE MAILED: 03/08/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

4/12

Office Action Summary	Application No. 10/690,246	Applicant(s) CHEN ET AL.	
	Examiner Maria Teresa Samson	Art Unit 1638	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --
Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 26-January 2004.
 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 1-3, 7-26 and 30-35 is/are pending in the application.
 4a) Of the above claim(s) 4-6 and 27-29 is/are withdrawn from consideration.
 5) ☐ Claim(s) _____ is/are allowed.
 6) ☒ Claim(s) 1-3, 7-26 and 30-35 is/are rejected.
 7) ☐ Claim(s) _____ is/are objected to.
 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☒ The specification is objected to by the Examiner.
 10) ☒ The drawing(s) filed on 21 October 2003 is/are: a) ☐ accepted or b) ☒ objected to by the Examiner.
 Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
 Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
 a) ☐ All b) ☐ Some * c) ☐ None of:
 1. ☐ Certified copies of the priority documents have been received.
 2. ☐ Certified copies of the priority documents have been received in Application No. _____.
 3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).
 * See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- | | |
|---|---|
| 1) <input checked="" type="checkbox"/> Notice of References Cited (PTO-892) | 4) <input type="checkbox"/> Interview Summary (PTO-413)
Paper No(s)/Mail Date. _____ |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948) | 5) <input type="checkbox"/> Notice of Informal Patent Application (PTO-152) |
| 3) <input checked="" type="checkbox"/> Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)
Paper No(s)/Mail Date _____ | 6) <input checked="" type="checkbox"/> Other: <u>see search notes</u> . |

DETAILED ACTION

Applicant's election without traverse of Group I, claims 1-26 and 30-35, and an isolated nucleic acid sequence of SEQ ID NO: 1 in the reply filed on 02-December 2004 is acknowledged. Claims 4-6, 27-29 and SEQ ID NOs: 3, 5 and 7 are withdrawn from consideration as being drawn to non-elected inventions.

Claims 1-3, 7-26 and 30-35 are examined on the merits to the extent that they are drawn to SEQ ID NO: 1.

Specification

(A.) The title of the invention is not descriptive of the instantly claimed invention, which is the DNA molecule encoding DEF-like MADS-box-genes from Phalaenopsis Orchid. A new title is required that is clearly indicative of the invention to which the claims are directed.

(B.) If applicant desires priority under 35 U.S.C. 111(a) based upon a previously filed application, specific reference to the earlier filed application must be made in the instant application. For benefit claims under 35 U.S.C. 120, 121 or 365(c), the reference must include the relationship (i.e., continuation, divisional, or continuation-in-part) of the applications. This should appear as the first sentence of the specification following the title, preferably as a separate paragraph unless it appears in an application data sheet. The status of nonprovisional parent application(s) (whether patented or abandoned) should also be included. If a parent application has become a patent, the expression "now Patent No. ____" should follow the filing date of the parent application. If a parent application has become abandoned, the expression "now abandoned" should follow the filing date of the parent application.

If the application is a utility or plant application filed under 35 U.S.C. 111(a) on or after November 29, 2000, the specific reference must be submitted during the pendency of the application and within the later of four months from the actual filing date of the application or sixteen months from the filing date of the prior application. If the application is a utility or plant application which entered the national stage from an international application filed on or after November 29, 2000, after compliance with 35 U.S.C. 371, the specific reference must be submitted during the pendency of the application and within the later of four months from the date on which the national stage commenced under 35 U.S.C. 371(b) or (f) or sixteen months from the filing date of the prior application. See 37 CFR 1.78(a)(2)(ii) and (a)(5)(ii). This time period is not extendable and a failure to submit the reference required by 35 U.S.C. 119(e) and/or 120, where applicable, within this time period is considered a waiver of any benefit of such prior application(s) under 35 U.S.C. 119(e), 120, 121 and 365(c). A priority claim filed after the required time period may be accepted if it is accompanied by a grantable petition to accept an unintentionally delayed claim for priority under 35 U.S.C. 119(e), 120, 121 and 365(c). The petition must be accompanied by (1) the reference required by 35 U.S.C. 120 or 119(e) and 37 CFR 1.78(a)(2) or (a)(5) to the prior application (unless previously submitted), (2) a surcharge under 37 CFR 1.17(t), and (3) a statement that the entire delay between the date the claim was due under 37 CFR 1.78(a)(2) or (a)(5) and the date the claim was filed was unintentional. The Director may require additional information where there is a question whether the delay was unintentional. The petition should be addressed to: Mail Stop Petition, Commissioner for Patents, P.O. Box 1450, Alexandria, Virginia 22313-1450.

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(C.) This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821 (a) (1) and (a) (2).

However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825.

Specifically, the sequences, PI-derived motif (FXFRLOPSQPNLH) and a paleoAP3 motif (YGXHDLRLA), in the specification (pg 8, lines 14 and 16 respectively) do not include sequence identifiers. Similarly, sequence identifiers are missing for the sequences in figures 2 and 3.

Full compliance with the sequence rules is required in response to this office action. A complete response to this office action must include both compliance with the sequence rules and a response to the issues set forth herein. Failure to fully comply with both of these requirements in the time period set forth in this office action will be held to be non-responsive.

(D.) The drawings are objected to because figure 1a-c is too dark and no details can be made out.

Claim Objections

Claims 1 and 4-6 are objected to because Claims 1 and 4-6 recite non-elected inventions claims 1 and 4-6 recite SEQ ID NOs other than SEQ ID NO: 1.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

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(A.) Claims 1-3, 7-26 and 30-35 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claims contain subject matter that was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claim is broadly drawn to a nucleic acid molecule that hybridizes to SEQ ID NO: 1, and said nucleic acid molecule is capable of controlling floral development in *Phalaenopsis*, a vector comprising the nucleic acid molecule that hybridizes to SEQ ID NO: 1, and said nucleic acid molecule is expressed, a kit comprising the vector, a cell transformed with the vector, a transgenic orchid comprising cells which contain a nucleic acid molecule that hybridizes to SEQ ID NO: 1, a transgenic orchid produced by transforming an orchid with the vector, a method for producing a transformed orchid cell comprising introducing a nucleic acid molecule that hybridizes to SEQ ID NO: 1, a protocorn-like body comprising a nucleic acid molecule that hybridizes to SEQ ID NO: 1, a method for producing a transgenic orchid comprising introducing a nucleic acid molecule that hybridizes to SEQ ID NO: 1, and regenerating the orchid transformed cell to obtain the transgenic orchid plant, a transgenic orchid produced by introducing a nucleic acid molecule that hybridizes to SEQ ID NO: 1 and regenerating the orchid transformed cell to obtain the transgenic orchid plant, a method for controlling floral development in orchid, which comprises providing an orchid plant with a nucleic acid molecule that hybridizes to SEQ ID NO: 1 and changing the amount of the protein.

Applicant does not describe a nucleic acid molecule that hybridizes to SEQ ID NO: 1, wherein said nucleic acid molecule is capable of controlling floral development in *Phalaenopsis*,

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a vector comprising the nucleic acid molecule that hybridizes to SEQ ID NO: 1, and said nucleic acid molecule is expressed, a kit comprising the vector, a cell transformed with the vector, a transgenic orchid comprising cells which contain a nucleic acid molecule that hybridizes to SEQ ID NO: 1, a transgenic orchid produced by transforming an orchid with the vector, a method for producing a transformed orchid cell comprising introducing a nucleic acid molecule that hybridizes to SEQ ID NO: 1, a protocorn-like body comprising a nucleic acid molecule that hybridizes to SEQ ID NO: 1, a method for producing a transgenic orchid comprising introducing a nucleic acid molecule that hybridizes to SEQ ID NO: 1, and regenerating the orchid transformed cell to obtain the transgenic orchid plant, a transgenic orchid produced by introducing a nucleic acid molecule that hybridizes to SEQ ID NO: 1 and regenerating the orchid transformed cell to obtain the transgenic orchid plant, a method for controlling floral development in orchid, which comprises providing an orchid plant with a nucleic acid molecule that hybridizes to SEQ ID NO: 1 and changing the amount of the protein.

Furthermore, there is no functional description of a nucleic acid molecule that hybridizes to SEQ ID NO: 1 that would control floral development in orchid. Applicant does not describe the sufficient structural elements of SEQ ID NO: 1 that are required for function and that these structural elements are also present in nucleic acid molecules that hybridize to SEQ ID NO: 1. The Applicant does not describe the sufficient structural elements of a representative number of nucleic acids that hybridize to SEQ ID NO: 1 and that will control floral development.

Hence, the specification fails to provide an adequate written description of the genus claimed.

Therefore, given the lack of written description in the specification with regard to the structural and functional characteristics of the claimed nucleic acids, it is not clear that Applicant was in possession of the claimed genus at the time this application was filed.

(B.) Claims 1-3, 7-26 and 30-35 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

The claims are drawn to SEQ ID NO: 1 and to a nucleic acid molecule that hybridizes to SEQ ID NO: 1, and said nucleic acid molecule is capable of controlling floral development in *Phalaenopsis*, a vector comprising the nucleic acid molecule that hybridizes to SEQ ID NO: 1, and said nucleic acid molecule is expressed, a kit comprising the vector, a cell transformed with the vector, a transgenic orchid comprising cells which contain a nucleic acid molecule that hybridizes to SEQ ID NO: 1, a transgenic orchid produced by transforming an orchid with the vector, a method for producing a transformed orchid cell comprising introducing a nucleic acid molecule that hybridizes to SEQ ID NO: 1, a protocorn-like body comprising a nucleic acid molecule that hybridizes to SEQ ID NO: 1, a method for producing a transgenic orchid comprising introducing a nucleic acid molecule that hybridizes to SEQ ID NO: 1, and regenerating the orchid transformed cell to obtain the transgenic orchid plant, a transgenic orchid produced by introducing a nucleic acid molecule that hybridizes to SEQ ID NO: 1 and regenerating the orchid transformed cell to obtain the transgenic orchid plant, a method for

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controlling floral development in orchid, which comprises providing an orchid plant with a nucleic acid molecule that hybridizes to SEQ ID NO: 1 and changing the amount of the protein.

Applicant's teachings only provide guidance for comparison of floral morphogenesis between wild type and peloric mutant (figure 1); identification of DEF-like MADS-box genes in *P. equestris* (pages 15-20), plant materials and RNA preparations (page 15); cDNA library construction (page 16); sequence data analysis (page 16); 5' rapid amplification of PeMADS cDNA ends (page 7); sequence alignments and construction of phylogenetic trees (page 18); isolation of genomic DNA and Southern blot analysis (page 20); RNA blot analysis (page 20); and differential expression profiles of the four PeMADS genes (page 21).

Applicant fails to provide guidance for how to use SEQ ID NO: 1, much less any a nucleic acid molecule that hybridizes to SEQ ID NO: 1, wherein said nucleic acid molecule is capable of controlling floral development in *Phalaenopsis*, a vector comprising the nucleic acid molecule of SEQ ID NO: 1 or that hybridizes to SEQ ID NO: 1, and said nucleic acid molecule is expressed, a kit comprising the vector, a cell transformed with the vector, a transgenic orchid comprising cells which contain a nucleic acid molecule of SEQ ID NO: 1 or that hybridizes to SEQ ID NO: 1, a transgenic orchid produced by transforming an orchid with the vector, a method for producing a transformed orchid cell comprising introducing a nucleic acid molecule of SEQ ID NO: 1 or that hybridizes to SEQ ID NO: 1, a protocorn-like body comprising a nucleic acid molecule of SEQ ID NO: 1 or that hybridizes to SEQ ID NO: 1, a method for producing a transgenic orchid comprising introducing a nucleic acid molecule of SEQ ID NO: 1 or that hybridizes to SEQ ID NO: 1, and regenerating the orchid transformed cell to obtain the transgenic orchid plant, a transgenic orchid produced by introducing a nucleic acid molecule of

SEQ ID NO: 1 or that hybridizes to SEQ ID NO: 1 and regenerating the orchid transformed cell to obtain the transgenic orchid plant, a method for controlling floral development in orchid, which comprises providing an orchid plant with a nucleic acid molecule of SEQ ID NO: 1 or that hybridizes to SEQ ID NO: 1 and changing the amount of the protein.

The specification does not teach making DNA molecules of SEQ ID NO: 1 or that hybridize to SEQ ID NO: 1 which can be used to control floral development in orchid. The specification does not exemplify transforming an orchid with SEQ ID NO: 1 to control floral development much less using any sequences that would hybridize to SEQ ID NO: 1. with the full scope of the claims and does not teach to make them.

It is well known to those skilled in the art that making substitutions in a nucleic acid does not produce predictable results. Lazar et al (1988, Mol. Cell. Biol. 8:1247-1252) showed that the “conservative” substitution of glutamic acid for aspartic acid at position 47 reduced biological function of transforming growth factor alpha while “nonconservative” substitutions with alanine or asparagine had no effect (abstract). Similarly, Hill et al (1998, Biochem. Biophys. Res. Comm. 244:573-577) teach that when three histidines that are maintained in ADP-glucose pyrophosphorylase across several species are substituted with the “nonconservative” amino acid glutamine, there is little effect on enzyme activity, while the substitution of one of those histidines with the “conservative” amino acid arginine drastically reduced enzyme activity (see Table 1).

In addition, the specification does not provide any guidance with regard to what structural features are required in a nucleic acid that can control floral development in orchid, and the

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claims are drawn to a multitude of sequences. Furthermore, there is no guidance with regard to how one would analyze transformed orchid plants for the control of floral development.

Given the claim breadth, unpredictability, and lack of guidance as discussed above, undue experimentation would have been required by one skilled in the art to develop and evaluate DEF-like genes-encoding nucleic acids that hybridize to SEQ ID NO: 1. Making all possible single amino acid substitutions in a 227 amino acid long protein like that encoded by SEQ ID NO: 1 would require making and analyzing 19^{227} nucleic acids; these proteins would have 99.6% identity to SEQ ID NO: 2. Because nucleic acids that hybridize to SEQ ID NO:1 could encode proteins with many amino acid substitutions, many more than 19^{227} nucleic acids would need to be made and analyzed. Guo et al. (2004, Proc. Natl. Acad. Sci. USA 101: 9205-9210) teach that while proteins are fairly tolerant to mutations resulting in single amino acid changes, increasing the number of substitutions additively increases the probability that the protein will be inactivated (pg 9209, right column, paragraph 2). Thus, making and analyzing proteins with many amino acid substitutions that also have DEF-like activity would require undue experimentation.

The claims also encompass plants transformed with a nucleic acid molecule of SEQ ID NO: 1 or that hybridizes to SEQ ID NO: 1. Yet, transforming plants with a heterologous rice MADS box gene leads to unpredictable results. Kang et al (1995, Plant Molecular Biology 29(1):1-10) teach transforming tobacco with the rice OsMADS3 nucleic acid sequence produced plants with altered morphology and coloration of the perianth organs. In some transgenic tobacco plants, the corolla (petals) resembled filaments (abstract). The specification does not teach how to use the plants transformed with a nucleic acid of SEQ ID NO: 1 or that hybridizes to SEQ ID NO: 1.

Furthermore, all of the four PeMADS genes isolated have characteristics in common with the DEF-like genes belonging to the class B floral homeotic genes. In the classical ABC model for flower development, expression of A genes specifies sepal formation in whorl 1 whereas the combination of class A and B genes specifies the formation of petals in whorl 2 and the combination of class B and C genes specify stamen formation in whorl 3. Thus, the PeMADS genes isolated should specify petal and stamen formation and not sepal formation. It is not clear how a B-class gene can specify sepal formation and the specification does not provide any examples of controlling sepal development with any of the claimed sequences.

Additionally, extensive further experimentation would be required to isolate and clone other nucleotide sequence that hybridizes to SEQ ID NO:1 and to determine whether the sequences are capable of controlling floral development specifically, sepal formation. The specification does not teach where to find such nucleotide sequence that hybridizes to SEQ ID NO:1 and does not teach how to make them.

Moreover, the specification does not teach how to use the method of controlling floral development in orchid by inducing, inhibiting and deleting the expression of the nucleic acid molecule and by increasing or decreasing the ploid of the nucleic acid molecule.

In an article entitled "A good antisense molecule is hard to find" Branch *et al.* sums up the challenges and unpredictability to finding effective antisense molecules (TIBS, vol. 23, Feb. 1998, pp. 45-50, attached). Branch teaches while antisense strategies look easy on paper, they are far more difficult to produce than was originally anticipated, and their ability to eliminate the function of a single gene has never been proven due to unexpected non-antisense effects and blocked internal structures rendering most potential binding sites inaccessible to antisense

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molecules (*ibid.* p. 45). Thus, transgenic plants comprising an antisense strand of a nucleic acid molecule that hybridizes to SEQ ID NO: 1 may not alter the amount of protein.

Further, the power of discrimination of an antisense fragment of at least 50 nucleotides in length is unpredictable because the mechanism of RNA knockout by antisense is sensitive to a short hybrid region as small as 10 base pairs or less of an RNA-RNA duplex for cleaving mRNA. Increases in size beyond this minimum region will not necessarily inhibit duplex formation, but may act to stabilize the structure, and thus the specificity of a short RNA fragment is dependent upon complex and unpredictable factors and will read on and eliminate messages other than that of its endogenous source and target. See Branch A.D. TIBS, February 1998, pages 45-50; page 47 column 3. Thus, hybridization encompasses sequences other than SEQ ID NO:1 and would therefore induce, inhibit and delete the expression of other proteins.

Thus, given the limited teachings and guidance by Applicant, the nature of the art and the unpredictability of the art, undue trial and error experimentation would have been required by one of skill in the art at the time of Applicant's invention to use the nucleic acid of SEQ ID NO: 1 and to screen through a myriad of nucleotide sequence that hybridizes to SEQ ID NO: 1 to find those that are DEF-like genes. Therefore, it would require undue experimentation for one skilled in the art to make/or use the claimed invention.

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

(A.) Claims 1, 31, 32 and 35 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Dependent claim is included in all rejections.

(1.) The term "hybridizes under stringent conditions" in claim 1 is a relative term which renders the claim indefinite, and the specification fails to define or clarify the use of this term.

(2.) In claims 8 and 35, "the nucleic acid molecule" in lines 2 and 3 respectively is indefinite. It is not clear what nucleic acid molecule is being referred to.

(3.) In claim 31, "inducing, inhibiting, and deleting" is indefinite. It is not clear how inducing, inhibiting and deleting can be accomplished at the same time.

(4.) In claim 32, "ploid" in line 2 is indefinite. The term should be defined within the claim.

(5.) In claim 1(f), the term "degeneration sequences" is unclear, and the specification fails to define or clarify the use of this term.

Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

Claim 21 is rejected under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter. The claim is drawn to a protocorn-like body, which is a product of nature.

Claim 21, as written, does not sufficiently distinguish over nucleic acids as they exist in nature because the claim does not particularly point out any non-naturally occurring differences

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between the claimed product and the naturally occurring product. In the absence of the hand of man, the naturally occurring products are considered non-statutory subject matter. See *American Wood v. Fiber Disintegrating Co.*, 90 U.S. 566 (1974), *American Fruit Growers v. Brogdex Co.*, 283 U.S. 2 (1931), *Funk Brothers Seed Co. v. Kalo Inoculant Co.*, 33 U.S. 127 (1948), *Diamond v. Chakrabarty*, 206 USPQ 193 (1980). It is suggested that the claim is modified to refer to the hand of the inventor, e.g. by replacing “comprising the nucleic acid molecule” in claim 21 with – comprising a vector comprising the nucleic acid molecule-- as taught by claim 7.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless --

(a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

(A.) Claim 1, 7-9, 11 and 14 are rejected under 35 U.S.C. 102 (e) as being anticipated by Strauss et al (U.S. Patent NO.: 6,395,892, effective filing date 1/October 1999).

Strauss et al teach a nucleotide sequence that hybridizes to SEQ ID NO: 1 because it has 58.3% similarity to it (See search results), and which is a floral homeotic gene that would control floral development, wherein the control of floral development in orchid would be inherent in the claimed sequence. Strauss et al also disclosed a cell comprising a vector comprising a nucleotide sequence that sequence that hybridizes to SEQ ID NO: 1 operably linked to an inducible promoter (column 17, lines 4 and 6; column 19 line 7).

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(B.) Claims 1, 7-8, 11 and 14 are rejected under 35 U.S.C. 102 (b) as being anticipated by Fernandez et al (U.S. Patent NO.: 6,133,435, 17/October 2000). Fernandez et al teach a nucleotide sequence that hybridizes to SEQ ID NO: 1 because it has 53.8% similarity to it (See search results), and controls floral development (column 12), wherein the control of floral development in orchid would be inherent in the claimed sequence.

Fernandez et al disclosed a cell comprising a vector comprising a nucleotide sequence that sequence that hybridizes to SEQ ID NO: 1 (column 10, line 51).

Claims 1a, 2-6, 10, 12-13, 15-26 and 30-35 are free of prior art given that the prior art of record does not teach or suggest SEQ ID NO: 1 or transformation of orchid cells or plants with the claimed sequence.

Conclusion

No claim is allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Maria Teresa Samson whose telephone number is 571-272-3110. The examiner can normally be reached on 7:00-5:00. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Amy Nelson, can be reached on 571-272-0804. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Patent applicants with problems or questions regarding electronic images that can be viewed in the Patent Application Information Retrieval system (PAIR) can now contact the USPTO's

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Patent Electronic Business Center (Patent EBC) for assistance. Representatives are available to answer your questions daily from 6 am to midnight (EST). The toll free number is (866) 217-9197. When calling please have your application serial or patent number, the type of document you are having an image problem with, the number of pages and the specific nature of the problem. The Patent Electronic Business Center will notify applicants of the resolution of the problem within 5-7 business days. Applicants can also check PAIR to confirm that the problem has been corrected. The USPTO's Patent Electronic Business Center is a complete service center supporting all patent business on the Internet. The USPTO's PAIR system provides Internet-based access to patent application status and history information. It also enables applicants to view the scanned images of their own application file folder(s) as well as general patent information available to the public. For all other customer support, please call the USPTO Call Center (UCC) at 800-786-9199.

Maria Teresa Samson, Ph.D
February 23, 2005


ELIZABETH MCELWAIN
PRIMARY EXAMINER

Thu Feb 3 15:54:19 2005

QY 128 AAGTACATATTTCTAAGAGAGAGTTGGATCTGAAGAAAGCCAAAGAGCTCAGTCTT 187
 DB 153 AAGTACATTTCTAAGAGAGAGTTGGATCTGAAGAAAGCTCAGTCTCAGTCTT 212
 QY 188 TCTGTGATGCTCAGTCTCTCATCATGTTCTCAAGCAGAGAAAGTTGGCTGATTACT 247
 DB 213 TCTGCATGCTGAGTGTGCTCATGCTCTTCTTCCAAAGGCAAACTTTGGAATATT 272
 QY 248 GAGAGCCCTCT 258
 DB 273 CCACCGACTCT 283

RESULT 13
 US-09-978-382A-1
 Sequence 1, Application US/0978382A.
 Patent No. 6781036
 GENERAL INFORMATION:
 APPLICANT: Yanofsky, Martin F.
 APPLICANT: Liljegen, Sarah
 TITLE OF INVENTION: The Regents of the University of California
 TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
 FILE REFERENCE: 19452A-000930US
 CURRENT APPLICATION NUMBER: US/09/978,382A
 PRIOR APPLICATION NUMBER: 2002-06-18
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: US 09/339,998
 PRIOR FILING DATE: 1999-06-25
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: Patent Ver. 2.1
 SEQ ID NO: 1
 LENGTH: 1062
 TYPE: DNA
 ORGANISM: Arabidopsis sp.
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (101)..(829)
 OTHER INFORMATION: AGAMOUS-Like 8 (AGL8)
 US-09-978-382A-1

Query Match 10.5%; Score 96.6; DB 4; Length 1062;
 Best Local Similarity 69.1%; Pred. No. 1.2e-16;
 Matches 134; Conservative 0; Mismatches 59; Indels 0; Gaps 0;
 QY 68 AGAGAGATGGGAGGAGGAGATAGATATAAAGATAGAGATCCGACAGACAGGC 127
 DB 93 AGAGAGATGGGAGGAGGAGGATGAGCTGAAGAGATAGAGAAACAAATGATGAGC 152
 QY 128 AAGTACATATTTCTAAGAGAGAGTTGGATCTGAAGAGCCAAAGAGCTCAGTCTT 187
 DB 153 AAGTACATTTCTAAGAGAGAGTTGGATCTGAAGAAAGCTCATGATCTCTTTC 212
 QY 188 TCTGTGATGCTCAGTCTCTCATCATGTTCTCAAGCAGAGAAAGTTGGCTGATTACT 247
 DB 213 TCTGCATGCTGAGTGTGCTCATGCTCTTCTTCCAAAGGCAAACTTTGGAATATT 272
 QY 248 GAGAGCCCTCT 258
 DB 273 CCACCGACTCT 283

RESULT 14
 US-08-904-284-6
 Sequence 6, Application US/08904284
 Patent No. 6133435
 GENERAL INFORMATION:
 APPLICANT: Fernandez, Donna E.
 APPLICANT: Heck, Gregory R.
 TITLE OF INVENTION: EXPRESSION OF AGL15 SEQUENCE IN
 TITLE OF INVENTION: TRANSGENIC PLANTS

NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Quarles & Brady
 STREET: 1 South Pinckney Street
 CITY: Madison
 STATE: WI
 COUNTRY: US
 ZIP: 53701-2113
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/904,284
 FILING DATE:
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Seay, Nicholas J.
 REGISTRATION NUMBER: 27,386
 REFERENCE/DOCKET NUMBER: 960296.94193
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (608) 251-5000
 TELEFAX: 608-251-9166
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2437 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-904-284-6

Query Match 10.4%; Score 95; DB 3; Length 2437;
 Best Local Similarity 69.9%; Pred. No. 4.8e-16;
 Matches 128; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
 QY 69 GAGAGAGATGGGAGGAGGAGATAGATATAAAGATAGAGATCCGACGAAACAGGCA 128
 DB 520 GGGGAAAATAGGATCTGTGAAAATAGATAGAGATCGAATGCGAATAGCAGACGA 579
 QY 129 AAGTACATATTTCTAAGAGAGAGTTGGATCTGAAGAGCCAAAGAGCTCAGTCTT 188
 DB 580 AAGTACATTTCTAAGAGAGGCTTCTGAGTACTTAAGAAAGCTCGTGAAGCTCTCTTCT 639
 QY 189 CTGTATCTCAGGCTCTCTCATCATGTTCTCAAGCAGAGAAAGTTGGCTGATTACT 248
 DB 640 TTGTGATGCTGAAGTTGCTCATGCTCTTCTTAAGTCTGCAAGCTCTTGAATCTC 699
 QY 249 CAG 251
 DB 700 CAG 702

RESULT 15
 US-08-904-284-2
 Sequence 2, Application US/08904284
 Patent No. 6133435
 GENERAL INFORMATION:
 APPLICANT: Fernandez, Donna E.
 APPLICANT: Heck, Gregory R.
 TITLE OF INVENTION: EXPRESSION OF AGL15 SEQUENCE IN
 TITLE OF INVENTION: TRANSGENIC PLANTS
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Quarles & Brady
 STREET: 1 South Pinckney Street
 CITY: Madison
 STATE: WI
 COUNTRY: US
 ZIP: 53701-2113
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/904,284
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296.94193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: 608-251-9156
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 795 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-904-284-2

Query Match 10.1%; Score 93; DB 3; Length 795;
Best Local Similarity 53.8%; Pred. No. 9.8e-16;
Matches 245; Conservative 0; Mismatches 195; Indels 15; Gaps 2;

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DB 61 TTCCTCAAGAGCGCTGCTGTTGCTCAAGAAAGCTCATGAGCTCTGTTCTTTGTAC 120
QY 196 GCTCAGGTCCTCATCATGATGTTCTCAAGACACAGAAAGTGGCTGATTAAGTCAAGCCCC 255
DB 121 GCTGAGGTTGCCGTCATGTTGTTCTTCCAAAGTCTGCAAGCTCTTGAGTTCTCAAGTACT 180
QY 256 TCTACTGATATTA-----AGGGATATATGAGAGGTACCAAGTTGTGACTGGA 303
DB 181 AGCATGAAGAAACACTTTGAGATACGGAATATTCAGATCTTTCAGATGTTCTGCG 240
QY 304 ATGATCTATGGAATGCTCAGTATGAGAGATGCAATAACGTTGAAGCATCTGAATAG 363
DB 241 AT--TAACTGTAAACAGAGAACAGAGAGGTGTACAGAGGTGACCTTTTAAAGAT 297
QY 364 ATTAACCAAAACCTGAGGAAGGAGATTAGAGAGAGAAAGGGGGAATTGAGAGCATG 423
DB 298 GAGATCTCAATGCTTCAAGAGAAACATTACATGACGAGGTAAGCCCTTGAACCTTCTG 357
QY 424 GACATAAAGCAACTGCGGGCTTGTAGCAAACTTGAAGAGTCTTTAGATTTAGG 483
DB 358 AGCTTGAAGAGCTGCAACACCTTGAGAGCACTAAATTTCTCATGATATCTGTGAGA 417
QY 484 CATGAAAGTATCATGTGATGCGCAACAACAACTGA 518
DB 418 GAGCGAAAGAACTATTGTGACTTAAACAACCTTGA 452

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Perfect score: 917

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scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

total number of hits satisfying chosen parameters: 1649014

Maximum DB seq length: 20000000000

Post-processing:	Minimum Match	0%
Maximum Match	100%	

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:

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4: /cgn2_6/prodata/1/ina/6B COMB.seq.*
5: /cgn2_6/prodata/1/ina/PCtUS COMB.seq.*
6: /cgn2_6/prodata/1/ina/backfile1.seq.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	228	24.9	946	3	US-09-410-444-2	Sequence 2, Appl
2	227.2	24.8	681	3	US-09-410-464-3	Sequence 1, Appl
3	109.4	11.9	4285	3	US-09-410-464-1	Sequence 1, Appl
4	101.8	11.1	1180	2	US-08-867-087B-16	Sequence 16, Appl
5	98.4	10.7	945	2	US-08-485-981-9	Sequence 9, Appl
6	98.4	10.7	945	2	US-08-867-087B-10	Sequence 10, Appl
7	96.8	10.6	1070	3	US-08-904-284-1	Sequence 1, Appl
8	96.6	10.5	1062	3	US-09-067-800-1	Sequence 1, Appl
9	96.6	10.5	1062	3	US-09-105-652-1	Sequence 1, Appl
10	96.6	10.5	1062	3	US-09-349-677-1	Sequence 1, Appl
11	96.6	10.5	1062	3	US-09-708-584-1	Sequence 1, Appl
12	96.6	10.5	1062	4	US-09-081-584-1	Sequence 1, Appl
13	96.6	10.5	1062	4	US-09-081-584-1	Sequence 1, Appl
14	95	10.4	2437	4	US-09-078-382A-1	Sequence 6, Appl
15	93	10.1	795	3	US-08-504-284-6	Sequence 2, Appl
16	91.6	10.0	2679	3	US-08-504-284-2	Sequence 4, Appl
17	91	9.9	798	4	US-08-504-284-2	Sequence 4, Appl
18	91	9.9	1010	4	US-09-611-659A-3	Sequence 3, Appl
19	91	9.9	1059	4	US-09-611-659A-2	Sequence 2, Appl
20	91	9.8	6701	4	US-08-867-087B-14	Sequence 14, Appl
21	89.6	9.8	1141	4	US-09-611-655A-1	Sequence 1, Appl
22	89.6	9.8	1141	2	US-08-323-445B-1	Sequence 1, Appl
23	89.6	9.8	1141	2	US-08-485-981-1	Sequence 1, Appl
24	89	9.7	4816	1	US-08-867-087B-1	Sequence 1, Appl
25	89	9.7	4816	1	US-08-592-214A-2	Sequence 22, Appl
26	88.8	9.7	779	3	US-09-149-976-22	Sequence 22, Appl
27	88.8	9.7	779	3	US-08-593-214A-9	Sequence 9, Appl

28	88.8	9.7	779	3	US-08-655-227-9	Sequence 9, Appl1
29	88.8	9.7	779	3	US-08-655-224-9	Sequence 9, Appl1
30	88.8	9.7	779	3	US-09-149-976-9	Sequence 9, Appl1
31	88.8	9.7	779	3	US-09-399-326-9	Sequence 9, Appl1
32	88.8	9.7	959	3	US-09-067-800-7	Sequence 7, Appl1
33	88.8	9.7	959	3	US-09-346-677-7	Sequence 7, Appl1
34	88.8	9.7	959	4	US-09-981-077-5	Sequence 5, Appl1
35	88.8	9.7	959	4	US-09-978-382A-5	Sequence 5, Appl1
36	88.8	9.7	555	4	US-08-159-976-20	Sequence 20, Appl1
37	88.8	9.7	555	1	US-08-592-214A-20	Sequence 20, Appl1
38	88.8	9.7	555	3	US-09-067-800-4	Sequence 20, Appl1
39	88.8	9.7	6138	3	US-09-349-677-4	Sequence 4, Appl1
40	88.6	9.7	6138	3	US-08-861-087B-54	Sequence 54, Appl1
41	87.8	9.5	1043	2	US-08-867-087A-12	Sequence 12, Appl1
42	87.4	9.5	794	1	US-08-592-214A-3	Sequence 3, Appl1
43	87.4	9.5	794	4	US-08-659-188-3	Sequence 3, Appl1
44	87.4	9.5	794	3	US-08-655-227-3	Sequence 3, Appl1
45	87.4	9.5	794	3	US-08-655-241-3	Sequence 3, Appl1

ALIGNMENTS

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RESULT 1
US-09-410-464-2
; Sequence 2, Application US/09410464
; Patent No. 635892
; GENERAL INFORMATION:
; APPLICANT: Straus et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; TITLE OF INVENTION: poplar and other plant species.
; FILE REFERENCE: 53375
; CURRENT APPLICATION NUMBER: US/09/410,464
; CURRENT FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: 09/287,700
; EARLIER FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,851
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2

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; NAME/KEY: CDS
; LOCATION: (1) .. (684)
US-09-410-464-2

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Query Match	24.9%	Score 228;	DB 3;	Length 946;
Best Local Similarity	58.3%	Pred. No. 1.6e-52;		
Matches 399; Conservative	0;	Mismatches 207		

	0; Mismatches	285;	Indels	0;	Gaps	0
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135

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Db
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316 ATGTCCTAGATGAGAGGATCAGAAATACCTCGAAGCATCTGAATGAGATTAAACCAAAAC 375

241 GGCACTCAATACGAGAAATGCAAGACACTTGAGGAGCTGAATGATATCAATCATTAAG 300

QY 376 CTGAGGAAGAGATTGAGAGAGAGAGGAGGAGGAAATTGAGGCGCATGAGCAATAAGCAA 435
 DB 301 CTGAGACAAAGAAATAGGACAGAGAGAGAGGCGCTGAAATGATCTAGACATTGATCAT 360
 QY 436 CTGCGCGGCTTGAGCAAACTTTGGAAGAGTCTTTAGAAATTTGTTAGGCATAGAAAGTAT 495
 DB 361 CTGCGCGGCTTGAGCAAACTTTGGAAGAGTCTTTAGAAATTTGTTAGGCATAGAAAGTAT 420
 QY 496 CATGTGATCGCCACAACTGACACTTACAAAGAAAGCTTTAAAGCAAGGAAACT 555
 DB 421 CATGTGATCGCCACAACTGACACTTACAAAGAGGAGTGAAGAAATTTAGAGAGAGA 480
 QY 556 TACCGCGCTTAATACATGATGATATGAAAGAGAGAAATCCGAACCTAGAGGTTTAT 615
 DB 481 CATGGAAGCTCTTGATGAAATATGAAAGCAAACTAGAGAGATGACAGATATGTTAGTG 540
 QY 616 GTAGAAAACAGAGTGAATTTATGAAATTCGATTCGAATGATGAAATGATGCTGAG 675
 DB 541 GCAATGAGAGCTGCTTGCACTTGCAAAATGGGCGCTTCAACCTCATGATCCGCGTG 600
 QY 676 ATGTTTCTTTAGGCTTTCATCCGAATCAGCCCAATCTGCTTGTAGTTATGAA 735
 DB 601 CATCAGGCGACACACCACCACTCTCCCTAATCTTCACTTGAGATGATGATTTGA 660
 QY 736 TCACATGATCTTAGCCTTGCAATTA 759
 DB 661 GCCCATGAACCTTCGCTTCTTGA 684

RESULT 2

US-09-410-464-3
 ; Sequence 3, Application US/09410464
 ; Patent No. 6395892
 ; GENERAL INFORMATION:
 ; APPLICANT: Straus et al.
 ; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
 ; TITLE OF INVENTION: poplar and other plant species.
 ; FILE REFERENCE: 53375
 ; CURRENT APPLICATION NUMBER: US/09/410,464
 ; CURRENT FILING DATE: 1999-10-01
 ; EARLIER APPLICATION NUMBER: 09/287,700
 ; EARLIER FILING DATE: 1999-04-06
 ; EARLIER APPLICATION NUMBER: 60/080,851
 ; EARLIER FILING DATE: 1998-04-06
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 681
 ; TYPE: DNA
 ; ORGANISM: Populus balsamifera subsp. trichocarpa
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1) .. (681)
 ; US-09-410-464-3

Query Match 24.8%; Score 227.2; DB 3; Length 681;
 Best Local Similarity 58.4%; Pred. No. 2.2e-52;
 Matches 397; Conservative 0; Mismatches 283; Indels 0; Gaps 0;

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 DB 1 ATGGGTCGTGAAAGATGAAATCAAGAGATCGAAAAACCCCAAAACAGGCAAGTACC 60
 QY 136 TATTTCTAAGAGAGAGTTGGAGTACTGAAGAAAGCCAGAGCTCAGTCTCTGTGAT 195
 DB 61 TACTGAAAGAGAGAGAGTTGATTTTCAAGAAAGCCCAAGAACTCAGTACTTGTGAT 120
 QY 196 GCTGAGCTCTCTCATGATGTTCTCAAGCAAGGAAAGTTGGCTGATTAAGTACGAGCCC 255
 DB 121 GCTAAGGCTCTCTTATCATGTTCTTCAACACTTAACAACTCAATGATTAAGCCCC 180
 QY 256 TCTACTGATATTAAAGGAGATATATGAGAGTACCAAGTTGTGATGATGATGATTTAG 315

DB 181 TCCACATCGACAAAGAGATCTACATCAATATCAGAACCTTTAGGCATAGATCTGTG 240
 QY 316 ATGCTCAGATGAGAGATGAGAAATACGCTGAGACATCTGAATGATTAACAAAC 375
 DB 241 GGCATCTATACAGAGAAATGCAAGAGCACTTAGAGAGCTGAATGATTAATCATTAAG 300
 QY 376 CTGAGGAAGAGATTGAGAGAGAGAGGAGGAGAAATTGAGAGGCAATGACATTAAGCAA 435
 DB 301 CTGAGAACAGAAATCAAGGACAGAGAGAGAGGCGCTGAAATGATCTGACATTAATCAT 360
 QY 436 CTGCGCGGCTTGAGCAAACTTTGGAAGAGTCTTTAGAAATTTGTTAGGCATAGAAAGTAT 495
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 QY 496 CATGTGATCGCCACAACTGACACTTACAAAGAAAGCTTTAAAGCAAGGAAACT 555
 DB 421 CATGTGATCGCCACAACTGACACTTACAAAGAGGAGTGAAGAAATTTAGAGAGAGA 480
 QY 556 TACCGCGCTTAATACATGAACTGATATGAAAGAGAGAAATCCGAACCTAGAGGTTTAT 615
 DB 481 CATGGAAGCTCTTGATGAAATATGAAAGCAAACTAGAGATGACAGATATGTTAGTG 540
 QY 616 GTAGAAAACAGAGTGAATTTATGAAATTCGATTCGAATGATGAAATGATGCTGAG 675
 DB 541 GCAATGAGAGCTGCTTGCACTTGCAAAATGGGCGCTTCAACCTCATGATTCGCGCTG 600
 QY 676 ATGTTTCTTTAGGCTTTCATCCGAATCAGCCCAATCTGCTTGTAGTTATGAA 735
 DB 601 CATCAGGCGACACACCACCACTCTCCCTAATCTTCACTTGAGATGATGATTTGA 660
 QY 736 TCACATGATCTTAGCCTTGCAATTA 755
 DB 661 GCCCATGAACCTTCGCTTCTTGA 680

RESULT 3

US-09-410-464-1
 ; Sequence 1, Application US/09410464
 ; Patent No. 6395892
 ; GENERAL INFORMATION:
 ; APPLICANT: Straus et al.
 ; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
 ; TITLE OF INVENTION: poplar and other plant species.
 ; FILE REFERENCE: 53375
 ; CURRENT APPLICATION NUMBER: US/09/410,464
 ; CURRENT FILING DATE: 1999-10-01
 ; EARLIER APPLICATION NUMBER: 09/287,700
 ; EARLIER FILING DATE: 1999-04-06
 ; EARLIER APPLICATION NUMBER: 60/080,851
 ; EARLIER FILING DATE: 1998-04-06
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 4285
 ; TYPE: DNA
 ; ORGANISM: Populus balsamifera subsp. trichocarpa
 ; US-09-410-464-1

Query Match 11.9%; Score 109.4; DB 3; Length 4285;
 Best Local Similarity 73.3%; Pred. No. 7.5e-20;
 Matches 140; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

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 QY 130 GTTACATATTTTAAAGAGAGAGTTGGAGTACTGAAGAGGCAAGAGAGCTCAGTCTC 189
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 DB 2115 TGTGATGCTAAGGCTCTCTTATCATGTTTCTCAACACTTAACAACTCAATGATGATTT 2174